```
    GAATTCGGCACGAGGTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTCTTTTCCTTTTGCC
1   ---------+---------+---------+---------+---------+---------+ 60

    ATCCGAAAGAGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAAC
61  ---------+---------+---------+---------+---------+---------+ 120

    AGTCAGAGACCCTCCTGAAAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGGCGG
121 ---------+---------+---------+---------+---------+---------+ 180

    CTGCGGCCCCTCCGTTCTTTCCCCCTCCCCGAGAGACACTCTTCCTTTCCCCCCACGAAG
181 ---------+---------+---------+---------+---------+---------+ 240

    ACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCCATGGGAGGCCGCTTCCTGCTGACG
241 ---------+---------+---------+---------+---------+---------+ 300

    CTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGCTCCGGGGTGTTCGAG
301 ---------+---------+---------+---------+---------+---------+ 360

    CTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGCTGCCGG
361 ---------+---------+---------+---------+---------+---------+ 420

    GGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTC
421 ---------+---------+---------+---------+---------+---------+ 480

    TGCCTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCC
481 ---------+---------+---------+---------+---------+---------+ 540

    ATCACCCCCGTCCTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGAC
541 ---------+---------+---------+---------+---------+---------+ 600

    CCCGCCTTCAGCAACCCCATCCGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCG
601 ---------+---------+---------+---------+---------+---------+ 660

    CTCATCATCGAGGCTCTGCACACCGACTCCCCCGACGACCTCACCACAGAAAACCCCGAG
661 ---------+---------+---------+---------+---------+---------+ 720

    CGCCTCATCAGCCGCCTGGCCACCCAGAGGCACCTGGCGGTGGGCGAGGAGTGGTCCCAG
721 ---------+---------+---------+---------+---------+---------+ 780

    GACCTGCACAGCAGCGGCCGCACCGACCTCAAGTACTCCTATCGCTTTGTGTGTGATGAG
781 ---------+---------+---------+---------+---------+---------+ 840
```

FIG. 1A1

```
     CACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGTCAC
841  ---------+---------+---------+---------+---------+---------+ 900

     TTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGC
901  ---------+---------+---------+---------+---------+---------+ 960

     ACTGAGCCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGG
961  ---------+---------+---------+---------+---------+---------+ 1020

     GAATGCAAGTGCAGAGTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCA
1021 ---------+---------+---------+---------+---------+---------+ 1080

     GGCTGCCTGCACGGTACCTGTCAGCAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGC
1081 ---------+---------+---------+---------+---------+---------+ 1140

     GGCCTTTTCTGCAACCAGGACCTGAACTACTGCACTCACCACAAGCCATGCAAGAATGGT
1141 ---------+---------+---------+---------+---------+---------+ 1200

     CGGTGTACGTGGTTGTGGCCAGTCCCCTCGATGTGAACAAGAACGGCTGGACCCATGTGT
1201 ---------+---------+---------+---------+---------+---------+ 1260

     GGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAGAATGGTGGA
1261 ---------+---------+---------+---------+---------+---------+ 1320

     AGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA
1321 ---------+---------+---------+---------+---------+---------+ 1380

     AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGC
1381 ---------+---------+---------+---------+---------+---------+ 1440

     ACTGACAACCCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAAC
1441 ---------+---------+---------+---------+---------+---------+ 1500

     TGTGAAAAGAAAATCGATTACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTT
1501 ---------+---------+---------+---------+---------+---------+ 1560

     GACCTGGGGAACTCCTACATATGCCAGTGCCAGGCTGGCTTCACTGGCAGGCACTGTGAC
1561 ---------+---------+---------+---------+---------+---------+ 1620

     GACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTCAATGGAGGGACCTGTCAGGATGGG
1621 ---------+---------+---------+---------+---------+---------+ 1680
```

FIG. 1A2

```
     GTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAGAACTGCAGCACGCCG
1681 ---------+---------+---------+---------+---------+---------+ 1740

     GTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGAAGCAAC
1741 ---------+---------+---------+---------+---------+---------+ 1800

     CGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCC
1801 ---------+---------+---------+---------+---------+---------+ 1860

     GAGCCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAAC
1861 ---------+---------+---------+---------+---------+---------+ 1920

     AGCCAGTTTCCCTGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTG
1921 ---------+---------+---------+---------+---------+---------+ 1980

     TACCAGTCGGTGTACGTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTG
2401 ---------+---------+---------+---------+---------+---------+ 2460

     TAAAACAGACGTGACGTGGCAAAGCTTATCGATACCGTCATCAAGCTT
2461 ---------+---------+---------+---------+-------- 2508
```

FIG. 1A3

```
   1 GAATTCGGCACGAGGTTTTTTTTTTTTTTTTTCCCCTCTTTTCTTTCTTTTCCTTTTGCCATCCGAAAG   69
  70 AGCTGTCAGCCGCCGCCGGGCTGCACCTAAAGGCGTCGGTAGGGGGATAACAGTCAGAGACCCTCCTGA  138
 139 AAGCAGGAGACGGGACGGTACCCCTCCGGCTCTGCGGGGCGGCTGCGGCCCCTCCGTTCTTTCCCCCTC  207
 208 CCCGAGAGACACTCTTCCTTTCCCCCCACGAAGACACAGGGGCAGGAACGCGAGCGCTGCCCCTCCGCC  276
 277 ATGGGAGGCCGCTTCCTGCTGACGCTCGCCCTCCTCTCGGCGCTGCTGTGCCGCTGCCAGGTTGACGGC  345
 346 TCCGGGGTGTTCGAGCTGAAGCTGCAGGAGTTTGTCAACAAGAAGGGGCTGCTCAGCAACCGCAACTGC  414
 415 TGCCGGGGGGGCGGCCCCGGAGGCGCCGGGCAGCAGCAGTGCGACTGCAAGACCTTCTTCCGCGTCTGC  483
 484 CTGAAGCACTACCAGGCCAGCGTCTCCCCCGAGCCGCCCTGCACCTACGGCAGCGCCATCACCCCCGTC  552
 553 CTCGGCGCCAACTCCTTCAGCGTCCCCGACGGCGCGGGCGGCGCCGACCCCGCCTTCAGCAACCCCATC  621
 622 CGCTTCCCCTTCGGCTTCACCTGGCCCGGCACCTTCTCGCTCATCATCGAGGCTCTGCACACCGACTCC  690
 691 CCCGACGACCTCACCACAGAAAACCCCGAGCGCCTCATCAGCCGCCTGGCCACCCAGAGGCACCTGGCG  759
 760 GTGGGCGAGGAGTGGTCCCAGGACCTGCACAGCAGCGGCCGCACCGACCTCAAGTACTCCTATCGCTTT  828
 829 GTGTGTGATGAGCACTACTACGGGGAAGGCTGCTCTGTCTTCTGCCGGCCCCGTGACGACCGCTTCGGT  897
 898 CACTTCACCTGTGGAGAGCGTGGCGAGAAGGTCTGCAACCCAGGCTGGAAGGGCCAGTACTGCACTGAG  966
 967 CCGATTTGCTTGCCTGGGTGTGACGAGCAGCACGGCTTCTGCGACAAACCTGGGGAATGCAAGTGCAGA 1035
1036 GTGGGTTGGCAGGGGCGGTACTGTGACGAGTGCATCCGATACCCAGGCTGCCTGCACGGTACCTGTCAG 1104
1105 CAGCCATGGCAGTGCAACTGCCAGGAAGGCTGGGGCGGCCTTTTCTGCAACCAGGACCTGAACTACTGC 1173
1174 ACTCACCACAAGCCATGCAAGAATGGTGCCACATGCACCAACACCGGTCAGGGGAGCTACACTTGTTCT 1242
1243 TGCCGACCTGGGTACACAGGCTCCAGCTGCGAGATTGAAATCAACGAATGTGATGCCAACCCTTGCAAG 1311
1312 AATGGTGGAAGCTGCACGGATCTCGAGAACAGCTATTCCTGTACCTGCCCCCCAGGCTTCTATGGTAAA 1380
1381 AACTGTGAGCTGAGTGCAATGACTTGTGCTGATGGACCGTGCTTCAATGGAGGGCGATGCACTGACAAC 1449
1450 CCTGATGGTGGATACAGCTGCCGCTGCCCACTGGGTTATTCTGGGTTCAACTGTGAAAAGAAAATCGAT 1518
1519 TACTGCAGTTCCAGCCCTTGTGCTAATGGAGCCCAGTGCGTTGACCTGGGGAACTCCTACATATGCCAG 1587
1588 TGCCAGGCTGGCTTCACTGGCAGGCACTGTGACGACAACGTGGACGATTGCGCCTCCTTCCCCTGCGTC 1656
1657 AATGGAGGGACCTGTCAGGATGGGGTCAACGACTACTCCTGCACCTGCCCCCCGGGATACAACGGGAAG 1725
1726 AACTGCAGCACGCCGGTGAGCAGATGCGAGCACAACCCCTGCCACAATGGGGCCACCTGCCACGAGAGA 1794
```

FIG. 1B1

1795 AGCAACCGCTACGTGTGCGAGTGCGCTCGGGGCTACGGCGGCCTCAACTGCCAGTTCCTGCTCCCCGAG 1863
1864 CCACCTCAGGGGCCGGTCATCGTTGACTTCACCGAGAAGTACACAGAGGGCCAGAACAGCCAGTTTCCC 1932
1933 TGGATCGCAGTGTGCGCCGGGATTATTCTGGTCCTCATGCTGCTGCTGGGTTGCGCCGCCATCGTCGTC 2001
2002 TGCGTCAGGCTGAAGGTGCAGAAGAGGCACCACCAGCCCGAGGCCTGCAGGAGTGAAACGGAGACCATG 2070
2071 AACAACCTGGCGAACTGCCAGCGCGAGAAGGACATCTCCATCAGCGTCATCGGTGCCACTCAGATTAAA 2139
2140 AACACAAATAAGAAAGTAGACTTTCACAGCGATAACTCCGATAAAAACGGCTACAAAGTTAGATACCCA 2208
2209 TCAGTGGATTACAATTTGGTGCATGAACTCAAGAATGAGGACTCTGTGAAAGAGGAGCATGGCAAATGC 2277
2278 GAAGCCAAGTGTGAAACGTATGATTCAGAGGCAGAAGAGAAAAGCGCAGTACAGCTAAAAAGTAGTGAC 2346
2347 ACTTCTGAAAGAAAACGGCCAGATTCAGTATATTCCACTTCAAAGGACACAAAGTACCAGTCGGTGTAC 2415
2416 GTCATATCAGAAGAGAAAGATGAGTGCATCATAGCAACTGAGGTTAGTATCCCACCTGGCAGTCGGACA 2484
2485 AGTCTTGGTGTGTGATTCCCATCCAGCGCAGGTCAGGGCGGCCAAACCATTCTACCTGCTGCCACAGTC 2553
2554 ATCTGTACCCAATGAAAACTGGCCACCTTCAGTCTGTGGCACTGCAGACGTTGAAAAAACTTGTTGTGG 2622
2623 ATTAACATAAGCTCCAGTGGGGGTTACAGGGACAGCAATTTTTGCAGGCAAGGGTATAACTGTAGTGCA 2691
2692 GTTGTAGCTTACTAACCCTACTGACTCATTCTTTCGTGTGCTTCCTGCAGAGCCTGTTTTTGCTTGGCA 2760
2761 TTGAGGTGAAGTCCTGACCCTCTGCATCCTCATAGTCCTCTGCTTTCTTTTTATTAACCTCTTCTGGTC 2829
2830 TCTGCTTGTGTTTTCTCTCAACAGGTGTAAAACAGACGTGACGTGGCAAAGCTT 2883

FIG. 1B2

1 MGGRFLLTLA LLSALLCRCQ VDGSGVFELK LQEFVNKKGL LSNRNCCRGG GPGGAGQQQC
61 DCKTFFRVCL KHYQASVSPE PPCTYGSAIT PVLGANSFSV PDGAGGADPA FSNPIRFPFG
121 FTWPGTFSLI IEALHTDSPD DLTTENPERL ISRLATQRHL AVGEEWSQDL HSSGRTDLKY
181 SYRFVCDEHY YGEGCSVFCR PRDDRFGHFT CGERGEKVCN PGWKGQYCTE PICLPGCDEQ
241 HGFCDKPGEC KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT
301 HHKPCKNGAT CTNTGQGSYT CSCRPGYTGS SCEIEINECD ANPCKNGGSC TDLENSYSCT
361 CPPGFYGKNC ELSAMTCADG PCFNGGRCTD NPDGGYSCRC PLGYSGFNCE KKIDYCSSSP
421 CANGAQCVDL GNSYICQCQA GFTGRHCDDN VDDCASFPCV NGGTCQDGVN DYSCTCPPGY
481 NGKNCSTPVS RCEHNPCHNG ATCHERSNRY VCECARGYGG LNCQFLLPEP PQGPVIVDFT
541 EKYTEGQNSQ FPWIAVCAGI ILVLMLLLGC AAIVVCVRLK VQKRHHQPEA CRSETETMNN
601 LANCQREKDI SISVIGATQI KNTNKKVDFH SDNSDKNGYK VRYPSVDYNL VHELKNEDSV
661 KEEHGKCEAK CETYDSEAEE KSAVQLKSSD TSERKRPDSV YSTSKDTKYQ SVYVISEEKD
721 ECIIATEV

FIG. 2

C-Delta-1	1	MGGRFLLTLA-LLSALLCRCQVDGSGVFELKLQEFVNKKGLLSNRNCCRGGGPGGAGQQQC	60
X-Delta-1	1	MGQQRMLTLL-VLSAVL--CQISCSGLFELRLQEFVNKKGLLGNMNCCRPGSL--ASLQRC	56
Delta	1	--MHWIKCLLTAFICFTVIVQVHSSGSFELRLKYFSNDHGRDNEGRCCSGESDGATGKCLG	59
C-Delta-1	61	DCKTFFRVCLKHYQASVSPEPPCTYGSAITPVLGANSFSVPDGAGGADPAFSNPIRFPFGF	121
X-Delta-1	57	ECKTFFRICLKHYQSNVSPEPPCTYGGAVTPVLGTNSFVVPES-SNADPTFSNPIRFPFGF	116
Delta	60	SCKTRFRLCLKHYQATIDTTSQCTYGDVITPILGENSVNLTDAQRFQNKGFTNPIQFPFSF	120
C-Delta-1	122	TWPGTFSLIIEALHTDSPDDLTTENPERLISRLATQRHLAVGEEWSQDLHSSGRTDLKYSY	182
X-Delta-1	117	TWPGTFSLIIEAIHADSADDLNTENPERLISRLATQRHLTVGEQWSQDLHSSDRTELKYSY	177
Delta	121	SWPGTFSLIVEAWH-DTNNSGNARTNKLLIQRLLVQQVLEVSSEWKTNKSESQYTSLEYDF	180
C-Delta-1	183	RFVCDEHYYGEGCSVFCRPRDDRFGHFTCGERGEKVCNPGWKGQYCTEPICLPGCDEQHGF	243
X-Delta-1	178	RFVCDEYYYGEGCSDYCRPRDDAFGHFSCGERGEKLCNPGWKGLYCTEPICLPGCDEHHGY	238
Delta	181	RVTCDLNYYGSGCAKFCRPRDDSFGHSTCSETGEIICLTGWQGDYCHIPKCAKGCE--HGH	239
		DSL	
C-Delta-1	244	CDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKP	304
X-Delta-1	239	CDKPGECKCRVGWQGRYCDECIRYPGCLHGTCQQPWQCNCQEGWGGLFCNQDLNYCTHHKP	299
Delta	240	CDKPNQCVCQLGWKGALCNECVLEPNCIHGTCNKPWTCICNEGWGGLYCNQDLNYCTNHRP	300
		EGF1 EGF2	
C-Delta-1	305	CKNGATCTNTGQGSYTCSCRPGYTGSSCEIEINECDA--NPCKNGGSCTD---LENSYSCT	360
X-Delta-1	300	CENGATCTNTGQGSYTCSCRPGYTGSNCEIEVNECDA--NPCKNGGSCSD---LENSYTCS	355
Delta	301	CKNGGTCFNTGEGLYTCKCAPGYSGDDCENEIYSCDADVNPCQNGGTCIDEPHTKTGYKCH	361
		EGF3 EGF4	
C-Delta-1	361	CPPGFYGKNCELSAMTCADGPCFNG-----GRCTDNPDGGYSCRCPLGYSGFNCEKKIDYC	416
X-Delta-1	356	CPPGFYGKNCELSAMTCADGPCFNG-----GRCADNPDGGYICFCPGVYSGFNCEKKIDYC	411
Delta	362	CRNGWSGKMCEEKVLTCSDKPCHQGICRNVRPGLGSKGQGYQCECPIGYSGPNCDLQLDNC	422
		EGF5	

FIG. 3A

```
C-Delta-1  417 SSSPCANGAQCVDLGNSYICQCQAGFTGRHCDDNVDDCASFPCVNGGTCQDGVNDYSCTCP 477
X-Delta-1  412 SSNPCANGARCEDLGNSYICQCQEGFSGRNCDDNLDDCTSFPCQNGGTCQDGINDYSCTCP 472
Delta      423 SPNPCINGGSCQPSGK---CICPSGFSGTRCETNIDDCLGHQCENGGTCIDMVNQYRCQCV 480
               ----------EGF6----------------><----------------EGF7---------

C-Delta-1  478 PGYNGKNCSTPVSRCEHNPCHNGATCHERSNRYVCECARGYGGLNCQFLLPEPPQGP---- 534
X-Delta-1  473 PGYIGKNCSMPITKCEHNPCHNGATCHERNNRYVCQCARGYGGNNCQFLLPE--------- 524
Delta      481 PGFHGTHCSSKVDLCLIRPCANGGTCLNLNNDYQCTCRAGFTGKDCSVDIDECSSGPCHNG 541
               ----------><---------------EGF8---------------><-------------

C-Delta-1  535 ---------------------------VIVDFTE--KYTEGQNSQFPW--IAVCAGIILVL 564
X-Delta-1  525 ------------------------EKPVVVDLTE--KYTEGQSGQFPW--IAVCAGIVLVL 557
Delta      542 GTCMNRVNSFECVCANGFRGKQCDEESYDSVTFDAHQYGATTQARADGLANAQVVLIAVFS 602
               ---EGF9----------------->

C-Delta-1  565 MLLLGCAAIVVCVRLKVQKRHHQPEACRSETETMNNLANCQREKD--ISISVIGATQIKNT 623
X-Delta-1  558 MLLLGCAAVVVCVRVRVQKRRHQPEACRGESKTMNNLANCQREKD--ISVSFIGTTQIKNT 616
Delta      603 VAMPLVAVIAACVVFCMKRKRKRAQEKDNAEARKQNEQNAVATMHHNGSAVGVALASASMG 663
               -TM---------

C-Delta-1  624 NKKVDFHSD-NSDKNGYKVRYPSVDYNLVHELKNEDSVKEEHGKCEAKCETYDSEAEEKSA 683
X-Delta-1  617 NKKIDFLSESNNEKNGYKPRYPSVDYNLVHELKNEDSPKEERSKCEAKCSSNDSDSEDVNS 677
Delta      664 GKTGSNSGLTFDGGNPNIIKNTWDKSVN-NICASAAAAAAAAAADECLMYGGYVASVADN 723

C-Delta-1  684 -----VQLKSSDTSERK---------RPDSVYSTSKDTKYQSVYVISEEKDECIIATEV  728
X-Delta-1  678 -----VHSK-RDSSERR---------RPDSAYSTSKDTKYQSVYVISDEKDECIIATEV  721
Delta      724 NNANSDFCVAPLQRAKSQKQLNTDPTLMHRGSPAGTSAKGASGGGPGAAEGKRISVLGEGS 784

Delta      785 YCSQRWPSLAAAGVAGACSSQLMAAASAAGTDGTAQQQRSVVCGTPHM              832
```

FIG. 3B

```
C-Delta-1   184  V-CDEHYYGE GCSVFCRPRD DRFGHFTCGE RGEKVCNPGW KGQYC 228
Delta       182  VTCDLNYYGS GCAKFCRPRD DSFGHSTCSE TGEIICLTGW QGDYC 226
Serrate     235  VQCAVTYYNT TCTTFCRPRD DQFGHYACGS EGQKLCLNGW QGVNC 279
C-Serrate-1      VTCAEHYYGF GCNKFCRPRD DFFTHHTCDQ NGNKTCLEGW TGPEC

Apx-1       130  NLCSSNYHGK RCNRYCIAN- AKLHWE-CST HGVRRCSAGW SGEDC 172
Lag-2       120  VTCARNYFGN RCENFCDAHL AKAARKRCDA MGRLRCDIGW MGPHC 166
```

FIG. 4

FIG.5A

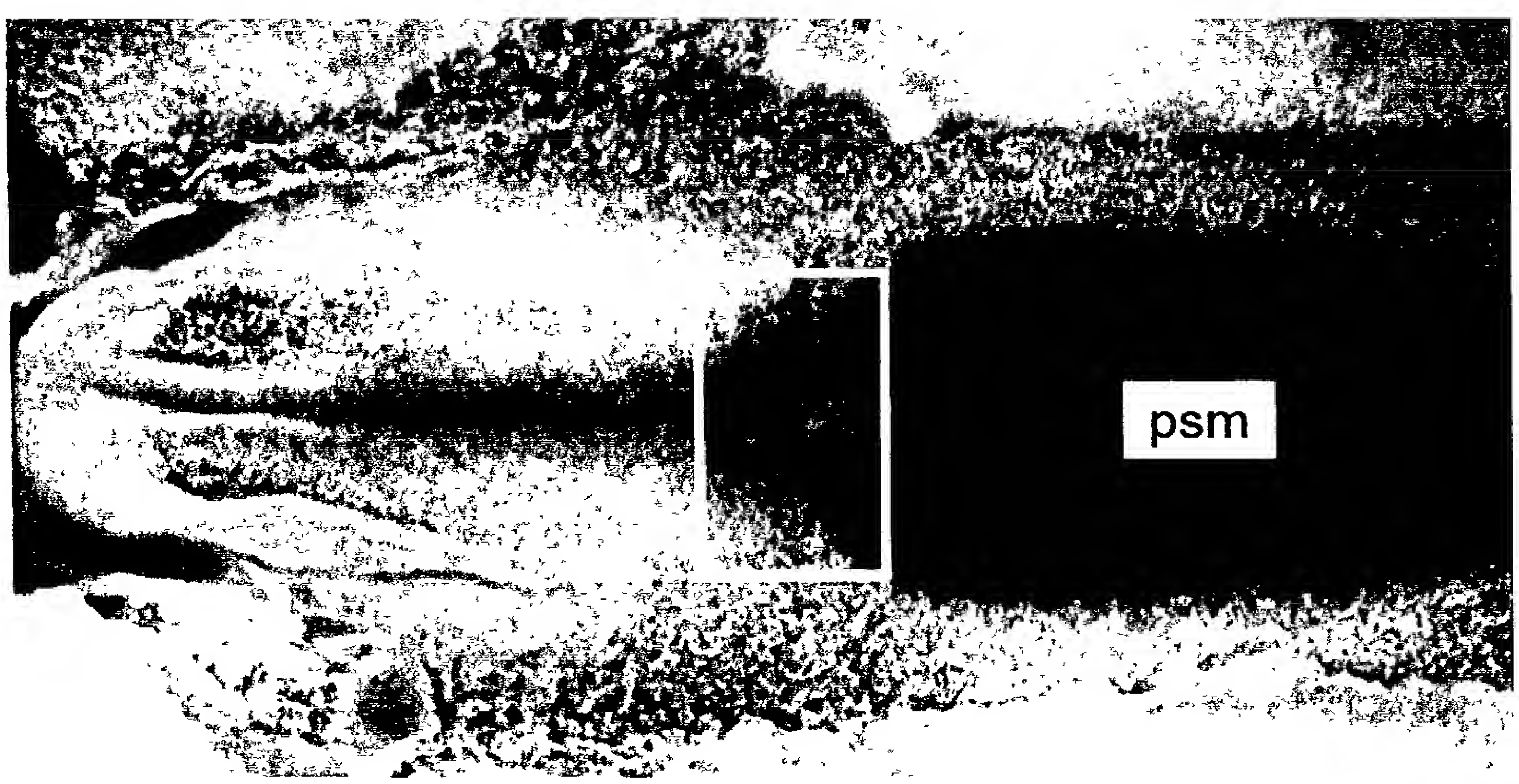

FIG.5B

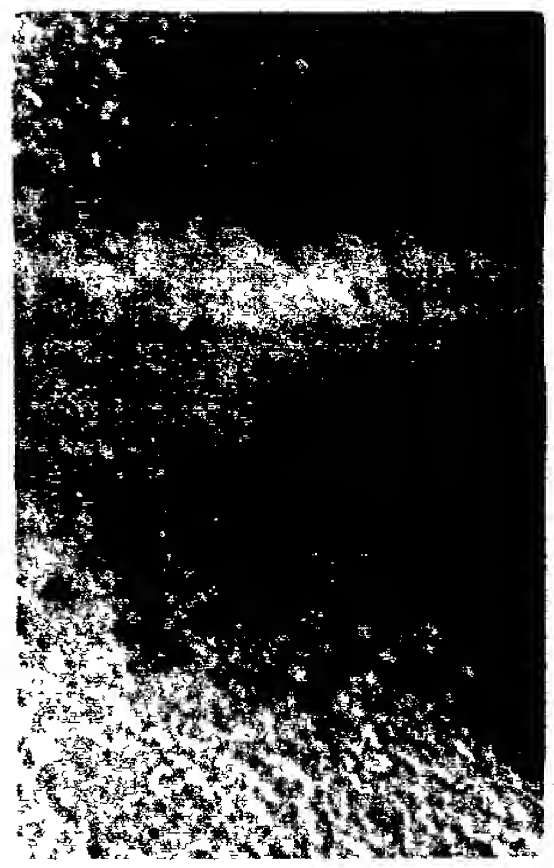

FIG.5C

FIG.5D

FIG.5E

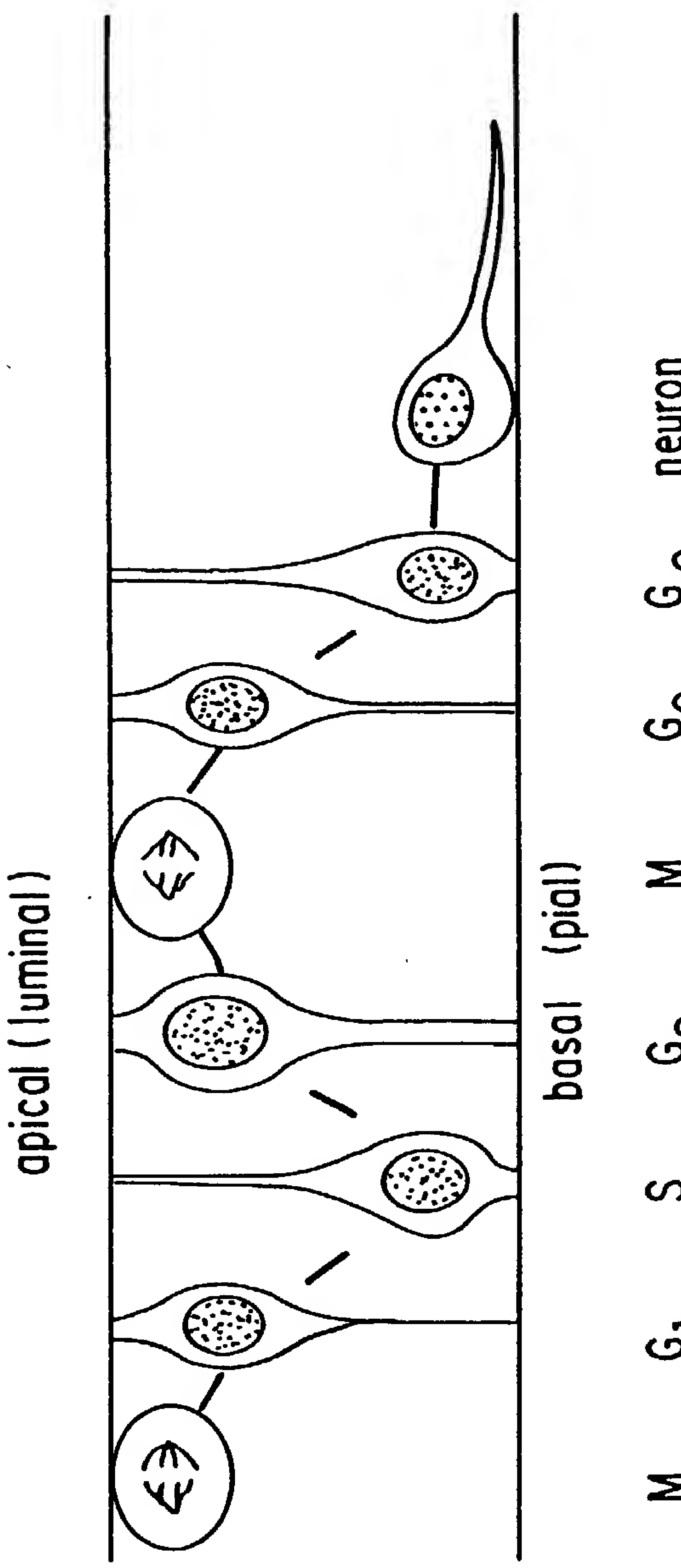

FIG. 6A

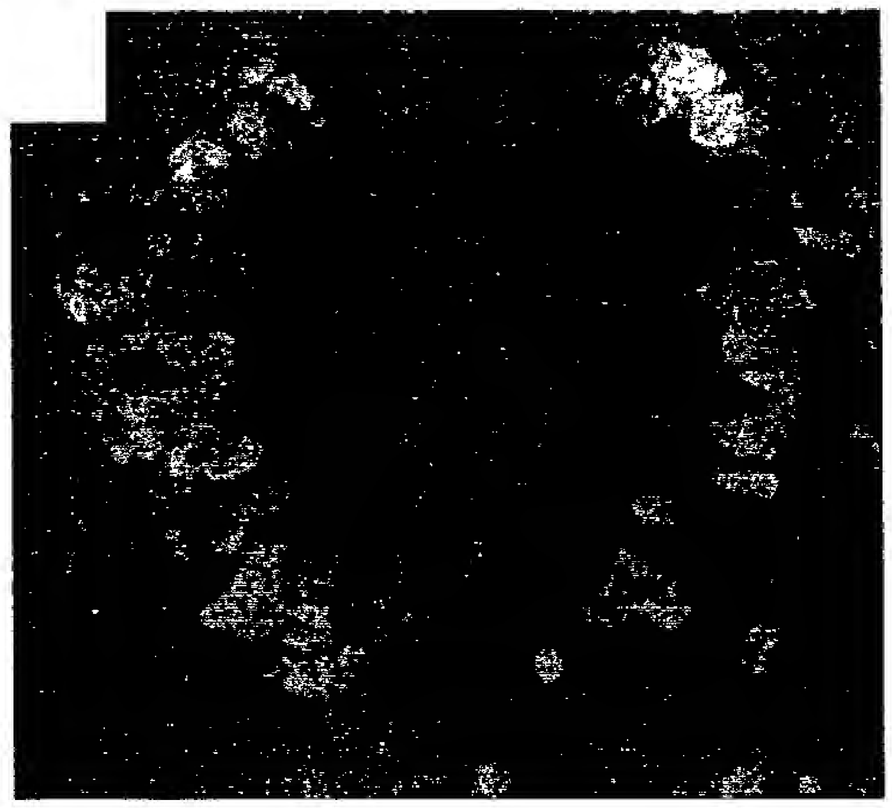

FIG.6B

FIG.6C

```
CTGCAGGAAT TCSMYCGCAT GCTCCCGGCC GCCATGGGCC GTCGGAGCGC GCTAGCCCTT   60
GCCGTGGTCT CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  120
CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG CGGGGGCTCT  180
GGCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC TCAAGCACTA CCAGGCCAGC  240
GTGTCACCGG AGCCACCCTG CACCTACGGC AGTGCCGTCA CGCCAGTGCT GGGTGTCGAC  300
TCCTTCAGCC TGCCTGATGG CGCAGGCATC GACCCCGCCT TCAGCAACCC CATCCGATTC  360
CCCTTCGGCT TCACCTGGCC AGGTACCTTC TCTCTGATCA TTGAAGCCCT CCATACAGAC  420
TCTCCCGATG ACCTCGCAAC AGAAAACCCA GAAAGACTCA TCAGCCGCCT GACCACACAG  480
AGGCACCTCA CTGTGGGAGA AGAATGGTCT CAGGACCTTC ACAGTAGCGG CCGCACAGAC  540
CTCCGGTACT CTTACCGGTT TGTGTGTGAC GAGCACTACT ACGGAGAAGG TTGCTCTGTG  600
TTCTGCCGAC CTCGGGATGA CGCCTTTGGC CACTTCACCT GCGGGGACAG AGGGGAGAAG  660
ATGTGCGACC CTGGCTGGAA AGGCCAGTAC TGCACTGACC CAATCTGTCT GCCAGGGTGT  720
GATGACCAAC ATGGATACTG TGACAAACCA GGGGAGTGCA AGTGCAGAGT TGGCTGGCAG  780
GGCCGCTACT GCGATGAGTG CATCCGATAC CCAGGTTGTC TCCATGGCAC CTGCCAGCAA  840
CCCTGGCAGT GTAACTGCCA GGAAGGCTGG GGGGGCCTTT TCTGCAACCA AGACCTGAAC  900
TACTGTACTC ACCATAAGCC GTGCAGGAAT GGAGCCACCT GCACCAACAC GGGCCAGGGG  960
AGCTACACAT GTTCCTGCCG ACCTGGGTAT ACAGGTGCCA ACTGTGAGCT GGAAGTAGAT 1020
GAGTGTGCTC CTAGCCCCTG CAAGAACGGA GCGAGCTGCA CGGACCTTGA GGACAGCTTC 1080
TCTTGCACCT GCCCTCCCGG CTTCTATGGC AAGGTCTGTG AGCTGAGCGC CATGACCTGT 1140
GCAGATGGCC CTTGCTTCAA TGGAGGACGA TGTTCAGATA ACCCTGACGG AGGCTACACC 1200
TGCCATTGCC CCTTGGGCTT CTCTGGCTTC AACTGTGAGA AGAAGATGGA TCTCTGCGGC 1260
TCTTCCCCTT GTTCTAACGG TGCCAAGTGT GTGGACCTCG GCAACTCTTA CCTGTGCCGG 1320
TGCCAGGCTG GCTTCTCCGG GAGGTACTGC GAGGACAATG TGGATGACTG TGCCTCCTCC 1380
```

FIG. 7A

```
CCGTGTGCAA ATGGGGGCAC CTGCCGGGAC AGTGTGAACG ACTTCTCCTG TACCTGCCCA   1440
CCTGGCTACA CGGGCAAGAA CTGCAGCGCC CCTGTCAGCA GGTGTGAGCA TGCACCCTGC   1500
CATAATGGGG CCACCTGCCA CCAGAGGGGC CAGCGCTACA TGTGTGAGTG CGCCCAGGGC   1560
TATGGCGGCC CCAACTGCCA GTTTCTGCTC CCTGAGCCAC CACCAGGGCC CATGGTGGTG   1620
GACCTCAGTG AGAGGCATAT GGAGAGCCAG GGCGGGCCCT TCCCCTGGGT GGCCGTGTGT   1680
GCCGGGGTGG TGCTTGTCCT CCTGCTGCTG CTGGGCTGTG CTGCTGTGGT GGTCTGCGTC   1740
CGGCTGAAGC TACAGAAACA CCAGCCTCCA CCTGAACCCT GTGGGGGAGA GACAGAAACC   1800
ATGAACAACC TAGCCAATTG CCAGCGCGAG AAGGACGTTT CTGTTAGCAT CATTGGGGCT   1860
ACCCAGATCA AGAACACCAA CAAGAAGGCG GACTTTCACG GGGACCATGG AGCCGAGAAG   1920
AGCAGCTTTA AGGTCCGATA CCCCACTGTG GACTATAACC TCGTTCGAGA CCTCAAGGGA   1980
GATGAAGCCA CGGTCAGGGA TACACACAGC AAACGTGACA CCAAGTGCCA GTCACAGAGC   2040
TCTGCAGGAG AAGAGAAGAT CGCCCCAACA CTTAGGGGTG GGGAGATTCC TGACAGAAAA   2100
AGGCCAGAGT CTGTCTACTC TACTTCAAAG GACACCAAGT ACCAGTCGGT GTATGTTCTG   2160
TCTGCAGAAA AGGATGAGTG TGTTATAGCG ACTGAGGTGT AAGATGGAAG CGATGTGGCA   2220
AAATTCCCAT TTCTCTTAAA TAAAATTCCA AGGATATAGC CCCGATGAAT GCTGCTGAGA   2280
GAGGAAGGGA GAGGAAACCC AGGGACTGCT GCTGAGAACC AGGTTCAGGC GAACGTGGTT   2340
CTCTCAGAGT TAGCAGAGGC GCCCGACACT GCCAGCCTAG GCTTTGGCTG CCGCTGGACT   2400
GCCTGCTGGT TGTTCCCATT GCACTATGGA CAGTTGCTTT GAAGAGTATA TATTTAAATG   2460
GACGAGTGAC TTGATTCATA TAGGAAGCAC GCACTGCCCA CACGTCTATC TTGGATTACT   2520
ATGAGCCAGT CTTTCCTTGA ACTAGAAACA CAACTGCCTT TATTGTCCTT TTTGATACTG   2580
AGATGTGTTT TTTTTTTTTC CTAGACGGGA AAAAGAAAAC GTGTGTTATT TTTTTTGGGA   2640
TTTGTAAAAA TATTTTTCAT GATTATGGGA GAGCTCCCAA CGCGTTGGAG GT           2692
```

FIG. 7B

MGRRSALALA	VVSALLCQVW	SSGVFELKLQ	EFVNKKGLLG	NRNCCRGGSG	50
PPCACRTFFR	VCLKHYQASV	SPEPPCTYGS	AVTPVLGVDS	FSLPDGAGID	100
PAFSNPIRFP	FGFTWPGTFS	LIIEALHTDS	PDDLATENPE	RLISRLTTQR	150
HLTVGEEWSQ	DLHSSGRTDL	RYSYRFVCDE	HYYGEGCSVF	CRPRDDAFGH	200
FTCGDRGEKM	CDPGWKGQYC	TDPICLPGCD	DQHGYCDKPG	ECKCRVGWQG	250
RYCDECIRYP	GCLHGTCQQP	WQCNCQEGWG	GLFCNQDLNY	CTHHKPCRNG	300
ATCTNTGQGS	YTCSCRPGYT	GANCELEVDE	CAPSPCKNGA	SCTDLEDSFS	350
CTCPPGFYGK	VCELSAMTCA	DGPCFNGGRC	SDNPDGGYTC	HCPLGFSGFN	400
CEKKMDLCGS	SPCSNGAKCV	DLGNSYLCRC	QAGFSGRYCE	DNVDDCASSP	450
CANGGTCRDS	VNDFSCTCPP	GYTGKNCSAP	VSRCEHAPCH	NGATCHQRGQ	500
RYMCECAQGY	GGPNCQFLLP	EPPPGPMVVD	LSERHMESQG	GPFPWVAVCA	550
GVVLVLLLLL	GCAAVVVCVR	LKLQKHQPPP	EPCGGETETM	NNLANCQREK	600
DVSVSIIGAT	QIKNTNKKAD	FHGDHGAEKS	SFKVRYPTVD	YNLVRDLKGD	650
EATVRDTHSK	RDTKCQSQSS	AGEEKIAPTL	RGGEIPDRKR	PESVYSTSKD	700
TKYQSVYVLS	AEKDECVIAT	EV			722

FIG. 8

```
CHICK DELTA      MGGRFLLTLA LLSALLCRCQ VDGSGVFELK LQEFVNKKGL LSNRNCCRGG 50
MOUSE DELTA.PEP  MGRRSALALA VVSALLCQ-- VWSSGVFELK LQEFVNKKGL LGNRNCCRGG 48

CONSENSUS        MG.R..L.LA ..SALLC... V..SGVFELD LQEFVNKKGL L.NRNCCRGG 50

CHICK DELTA      GPGGAGQQQC DCKTFFRVCL KHYQASVSPE PPCTYGSAIT PVLGANSFSV 100
MOUSE DELTA.PEP  --SGP---PC ACRTFFRVCL KHYQASVSPE PPCTYGSAVT PVLGVDSFSL 93

CONSENSUS        ...G.....C .C.TFFRVCL KHYQASVSPE PPCTYGSA.T PVLG..SFS. 100

CHICK DELTA      PDGAGGADPA FSNPIRFPFG FTWPGTFSLI IEALHTDSPD DLTTENPERL 150
MOUSE DELTA.PEP  PDGAG-IDPA FSNPIRFPFG FTWPGTFSLI IEALHTDSPD DLATENPERL 142

CONSENSUS        PDGAG..DPA FSNPIRFPFG FTWPGTFSLI IEALHTDSPD DL.TENPERL 150

CHICK DELTA      ISRLATQRHL AVGEEWSQDL HSSGRTDLKY SYRFVCDEHY YGEGCSVFCR 200
MOUSE DELTA.PEP  ISRLTTQRHL TVGEEWSQDL HSSGRTDLRY SYRFVCDEHY YGEGCSVFCR 192

CONSENSUS        ISRL.TQRHL .VGEEWSQDL HSSGRTDL.Y SYRFVCDEHY YGEGCSVFCR 200

CHICK DELTA      PRDDRFGHFT CGERGEKVCN PGWKGQYCTE PICLPGCDEQ HGFCDKPGEC 250
MOUSE DELTA.PEP  PRDDAFGHFT CGDRGEKMCD PGWKGQYCTD PICLPGCDDQ HGYCDKPGEC 242

CONSENSUS        PRDD.FGHFT CG.RGEK.C. PGWKGQYCT. PICLPGCD.Q HG.CDKPGEC 250

CHICK DELTA      KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT 300
MOUSE DELTA      KCRVGWQGRY CDECIRYPGC LHFTCQQPWQ CNCQEGWGGL FCNQDLNYCT 292

CONSENSUS        KCRVGWQGRY CDECIRYPGC LHGTCQQPWQ CNCQEGWGGL FCNQDLNYCT 300

CHICK DELTA      HHKPCKNGAT CTNTGQGSTY CSCRPGYTGS SCEIEINECD ANPCKNGGSC 350
MOUSE DELTA.PEP  HHKPCRNGAT CTNTGQGSYT CSCRPGYTGA NCELEVDECA PSPCKNGASC 342

CONSENSUS        HHKPC.NGAT CTNTGQGSYT CSCRPGYTG. .CE.E..EC. ..PCKNG.SC 350

CHICK DELTA      TDLENSYSCT CPPGFYGKNC ELSAMTCADG PCFNGGRCTD NPDGGYSCRC 400
MOUSE DELTA.PEP  TDLEDSFSCT CPPGFYGKVC ELSAMTCADG PCFNGGRCSD NPDGGYTCHC 392

CONSENSUS        TDLE.S.SCT CPPGFYGK.C ELSAMTCADG PCFNGGRC.D NPDGGY.C.C 400

CHICK DELTA      PLGYSGFNCE KKIDYCSSSP CANGAQCVDL GNSYICQCQA GFTGRHCDDN 450
MOUSE DELTA.PEP  PLGFSGFNCE KKMDLCGSSP CSNGAKCVDL GNSYLCRCQA GFSGRYCEDN 442

CONSENSUS        PLG.SGFNCE KK.D.C.SSP C.NGA.CVDL GNSY.C.CQA GF.GR.C.DN 450
```

FIG.9A

```
CHICK DELTA        VDDCASFPQV NGGTCQDGVN DYSCTCPPGY NGKNCSTPVS RCEHNPCHNG 500
MOUSE DELTA.PEP    VDDCASSPCA NGGTCRDSVN DFSCTCPPGY TGKNCSAPVS RCEHAPCHNG 492

CONSENSUS          VDDCAS.PC. NGGTC.D.VN D.SCTCPPGY .GKNCS.PVS RCEH.PCHNG 500

CHICK DELTA        ATCHERSNRY VCECARGYGG LNCQFLLPEP PQGPVIVDFT EKYTEGQNSQ 550
MOUSE DELTA        ATCHQRGQRY MCECAQGYGG PNCQFLLPEP PPGPMVVDLS ERHMESQGGP 542

CONSENSUS          ATCH.R..RY .CECA.GYGG .NCQFLLPEP P.GP..VD.. E...E.Q... 550

CHICK DELTA        FPWIAVCAGI ILVLMLLGCA AIVVCVRLKV QKRHHQPEAC RSETETMNN 600
MOUSE DELTA.PEP    FPWVAVCAGV VLVLLLLGCA AVVVCVRLKL QKHQPPPEPC GGETETMNN 592

CONSENSUS          FPW.AVCAG. .LVL.LLGCA A.VVCVRLK. QK....PE.C ..ETETMNN 600

CHICK DELTA        LANCQREKDI SISVIGATQI KNTNKKVDFH SDN-SDKNGY KVRYPSVDYN 649
MOUSE DELTA        LANCQREKDV SVSIIGATQI KNTNKKADFH GDHGAEKSSF KVRYPTVDYN 642

CONSENSUS          LANCQREKD. S.S.IGATQI KNTNKK.DFH .D....K... KVRYP.VDYN 650

CHICK DELTA        LVHELKNED- SVKEEHGKCE AKCETYDSEA EEKSAVQLKS SDTSERKRPD 698
MOUSE DELTA.PEP    LVRDLKGDEA TVRDTHSKRD TKCQSQSSAG EEKIAPTLRG GEIPDRKRPE 692

CONSENSUS          LV..LK.... .V...H.K.. .KC....S.. EEK.A..L.. .....RKRP. 700

CHICK DELTA        SVYSTSKDTK YQSVYVISEE KDECIIATEV 728
MOUSE DELTA.PEP    SVYSTSKDTK YQSVYVLSAE KDECVIATEV 722
CONSENSUS          SVYSTSKDTK YQSVYV.S.E KDEC.IATEV 730
```

FIG.9B

```
        10         20         30         40         50         60
         *          *          *          *          *          *
TACGATGAAY AACCTGGCGA ACTGCCAGCG TCAGAAGGAC ATCTCAGTCA GCATCATCGG
 Y  D  E   X  P  G  E   L  P  A   *  E  G   H  L  S  Q   H  H  R>
  T  M  N   N  L  A   N  C  Q  R   E  K  D   I  S  V   S  I  I  G>
   R  *  X   T  W  R   T  A  S   V  R  R  T   S  Q  S   A  S  S>

        70         80         90        100        110        120
                    *                     *                     *
GGCYACGTCA GATCARGAAC ACCAACAAGA AGGCGGACTT YMCASCGGGG GACCASAGCG
 G  X  V   R  S  X  T   P  T  R   R  R  T   X  X  R  G   T  X  A>
  A  T  S   D  Q  E   H  Q  Q  E   G  G  L   X  X  G   G  P  X  R>
G  X  R  Q   I  X  N   T  N  K   K  A  D  F   X  X  G   D  X  S>

       130        140        150        160        170        180
                    *                     *                     *
TCCGACAAGA ATGGMTTTCA AGGCCYGCTA CCCCAGCGTG GACTATAACT CGTGCAGGAC
 S  D  K   N  G  F  Q   G  P  L   P  Q  R   G  L  *  L   V  Q  D>
  P  T  R   M  X  F   K  A  R  Y   P  S  V   D  Y  N   S  C  R  T>
V  R  Q  E   W  X  S   R  P  A   T  P  A  W   T  I  T   R  A  G>

       190        200        210        220        230        240
                    *                     *                     *
CTCAAGGGTG ACGACACCGC CGTCAGGACG TCGCACAGCA AGCGTGACAC CAAGTGCCAG
 L  K  G   D  D  T  A   V  R  T   S  H  S   K  R  D  T   K  C  Q>
  S  R  V   T  T  P   P  S  G  R   R  T  A   S  V  T   P  S  A  S>
P  Q  G  *   R  H  R   R  Q  D   V  A  Q  Q   A  *  H   Q  V  P>

       250        260        270        280        290        300
                    *                     *                     *
TCCCCAGGCT CCTCAGGGAG GAGAAGGGGA CCCCGACCAC ACTCAGGGGK TGCGTGCTGC
 S  P  G   S  S  G  R   R  R  G   P  R  P   H  S  G  X   A  C  C>
  P  Q  A   P  Q  G   G  E  G  D   P  D  H   T  Q  G   X  R  A  A>
V  P  R  L   L  R  E   E  K  G   T  P  T  T   L  R  G   C  V  L>

       310        320        330        340        350        360
                    *                     *                     *
GGGCCGGGCT CAGGAGGGGG TACCTGGGGG GTGTCTTCCT GGAACCACTG CTCCGTTTCT
 G  P  G   S  G  G  G   T  W  G   V  S  S   W  N  H  C   S  V  S>
  G  R  A   Q  E  G   V  P  G  G   C  L  P   G  T  T   A  P  F  L>
R  A  G  L   R  R  G   Y  L  G   G  V  F  L   E  P  L   L  R  F>
```

FIG. 10A

```
        370        380        390        400        410        420
                     *                     *                     *
CTTCCCAAAT GTTCTCATGC ATTCATTGTG GATTTTCTCT ATTTTCCTTT TAGTGGAGAA
 L  P  K   C  S  H  A   F  I  V   D  F  L   Y  F  P  F   S  G  E>
  F  P  N   V  L  M   H  S  L  W   I  F  S   I  F  L   L  V  E  K>
S  S  Q  M  F  S  C    I  H  C   G  F  S  L   F  S  F   *  W  R>

       430        440        450        460        470        480
                     *                     *                     *
GCATCTGAAA GAAAAAGGCC GGACTCGGGC TGTTCAACTT CAAAAGACAC CAAGTACCAG
 A  S  E   R  K  R  P   D  S  G   C  S  T   S  K  D  T   K  Y  Q>
  H  L  K   E  K  G   R  T  R  A   V  Q  L   Q  K  T   P  S  T  S>
S  I  *  K   K  K  A   G  L  G  L   F  N  F   K  R  H   Q  V  P>

       490        500        510        520
                     *                     *
TCGGTGTACG TCATATCCGA GGAGAAGGAC GAGTGCGTCA TCGCA
 S  V  Y   V  I  S  E   E  K  D   E  C  V   I  A>
  R  C  T   S  Y  P   R  R  R  T   S  A  S   S>
V  G  V  R   H  I  R   G  E  G   R  V  R  H   R>
```

FIG. 10B

```
  1 TMNNLANCQREKDISVSIIGATQIXNTNKKADFXXGDXSSDKNGFQKARY  50
    |||||||||||||||:|:||||||||||||.|| ::   |||||: |.||
597 TMNNLANCQREKDISISVIGATQIKNTNKKVDFHSDN..SDKNGY.KVRY 643

 51 PSVDYNLVQDLKGDDTAVRTSHSKRDTKCQSPGSSGRRRGPRPHSGXACC 100
    ||||||||::||.:| .|:..|:| :.||: .:|.:  :::
644 PSVDYNLVHELKNED.SVKEEHGKCEAKCETYDSEAEEKSA.........  683

101 GPGSGGGTWGVSSWNHCSVSLPKCSHAFIVDFLYFPFSGEASERKRPDSG 150
                                 |::     |::.||||||||.
684 .............................VQLK....SSDTSERKRPDSV 700

151 CSTSKDTKYQSVYVISEEKDECVIA  175
    :|||||||||||||||||||||:||
701 YSTSKDTKYQSVYVISEEKDECIIA  725
```

FIG. 11

```
        10         20         30         40         50         60
    *    *     *    *     *    *     *    *     *    *     *    *
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG
        70         80         90        100        110        120
    *    *     *    *     *    *     *    *     *    *     *    *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA
       130        140        150        160        170        180
    *    *     *    *     *    *     *    *     *    *     *    *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT
       190        200        210        220        230        240
    *    *     *    *     *    *     *    *     *    *     *    *
GACGGTGGGC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA
       250        260        270        280        290        300
    *    *     *    *     *    *     *    *     *    *     *    *
CTCCTACCGC TTCGTGTGTC ACCAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG
       310        320        330        340        350        360
    *    *     *    *     *    *     *    *     *    *     *    *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA
       370        380        390        400        410        420
    *    *     *    *     *    *     *    *     *    *     *    *
CCCTGGCTCG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA
       430        440        450        460        470        480
    *    *     *    *     *    *     *    *     *    *     *    *
GCATGGATTT TGTGACAAAC CAGGGGAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA
       490        500        510        520        530        540
    *    *     *    *     *    *     *    *     *    *     *    *
GTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA
       550        560        570        580        590        600
    *    *     *    *     *    *     *    *     *    *     *    *
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC
       610        620        630        640        650        660
    *    *     *    *     *    *     *    *     *    *     *    *
ACACCATAAG CCCTGCAAGA ATGGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC
       670        680        690        700        710        720
    *    *     *    *     *    *     *    *     *    *     *    *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA
       730        740        750        760        770        780
    *    *     *    *     *    *     *    *     *    *     *    *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC
       790        800        810        820        830        840
    *    *     *    *     *    *     *    *     *    *     *    *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG
       850        860        870        880        890        900
    *    *     *    *     *    *     *    *     *    *     *    *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CAGACAGCCC CGATGGAGGG
```

FIG. 12A1

```
       910        920        930        940        950        960
         *    *     *    *     *    *     *    *     *    *     *    *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC
       970        980        990       1000       1010       1020
         *    *     *    *     *    *     *    *     *    *     *    *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG
      1030       1040       1050       1060       1070       1080
         *    *     *    *     *    *     *    *     *    *     *    *
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC
      1090       1100       1110       1120       1130       1140
         *    *     *    *     *    *     *    *     *    *     *    *
TCCTCCCCGT GCGCCAACGG ACCTCGGTGA CGGGATGGCG TGAACGACTT CTCCTGCACC
      1150       1160       1170       1180       1190       1200
         *    *     *    *     *    *     *    *     *    *     *    *
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCACCTG CGAGCACGCA
      1210       1220       1230       1240       1250       1260
         *    *     *    *     *    *     *    *     *    *     *    *
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGCACGCA
      1270       1280       1290       1300       1310       1320
         *    *     *    *     *    *     *    *     *    *     *    *
CGAAGCTACG GGGGTCCCAA CTCCCANTTC CTGCTCCCCC AAACTGCCCC CCCGGCCCCA
      1330       1340       1350       1360       1370       1380
         *    *     *    *     *    *     *    *     *    *     *    *
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT
      1390       1400       1410       1420       1430       1440
         *    *     *    *     *    *     *    *     *    *     *    *
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTG CCGCTGTGGT
      1450       1460       1470       1480       1490       1500
         *    *     *    *     *    *     *    *     *    *     *    *
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA
      1510       1520       1530       1540       1550       1560
         *    *     *    *     *    *     *    *     *    *     *    *
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT
      1570       1580       1590       1600       1610       1620
         *    *     *    *     *    *     *    *     *    *     *    *
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG
      1630       1640       1650       1660       1670       1680
         *    *     *    *     *    *     *    *     *    *     *    *
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA
      1690       1700       1710       1720       1730       1740
         *    *     *    *     *    *     *    *     *    *     *    *
CCTCAAGGGT GACGACACCG CCGTCAGCCA CGCGCACAGC AAGCGTGACA CCAAGTGNCA
      1750       1760       1770       1780       1790       1800
         *    *     *    *     *    *     *    *     *    *     *    *
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG
```

FIG.12A2

```
      1810      1820      1830      1840      1850      1860
         *    *    *    *    *    *    *    *    *    *    *    *
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA
      1870      1880      1890      1900      1910      1920
         *    *    *    *    *    *    *    *    *    *    *    *
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG
      1930      1940      1950      1960      1970      1980
         *    *    *    *    *    *    *    *    *    *    *    *
AGGTNGTAAA NTGGNAGTTG ANNTTGGAAA GNNNTCCCCG GATTCCGNTT TCAAAGTTTT

T
```

FIG. 12A3

```
        10        20        30        40        50        60
   *    *    *    *    *    *    *    *    *    *    *    *  a.a.no.
CATTGGGTAC GGGCCCCCCT CGAGGTCGAC GGTATCGATA AGCTTGATAT CGAATTCCGG
 H W V R A P L E V D G I D K L D I E F R>   20
 I G Y G P P S R S T V S I S L I S N S G>   20
 L G T G P P R G R R Y R * A * Y R I P>     19

        70        80        90       100       110       120
   *    *    *    *    *    *    *    *    *    *    *    *
CTTCACCTGG CCGGGCACCT TCTCTCTGAT TATTGAAGCT CTCCACACAG ATTCTCCTGA
 L H L A G H L L S D Y * S S P H R F S *>   40
 F T W P G T F S L I I E A L H T D S P D>   40
 A S P G R A P S L * L L K L S T Q I L L>   39

       130       140       150       160       170       180
   *    *    *    *    *    *    *    *    *    *    *    *
TGACCTCGCA ACAGAAAACC CAGAAAGACT CATCAGCCGC CTGGCCACCC AGAGGCACCT
 * P R N R K P R K T H Q P P G H P E A P>   60
 D L A T E N P E R L I S R L A T Q R H L>   60
 M T S Q Q K T Q K D S S A A W P P R G T>   59

       190       200       210       220       230       240
   *    *    *    *    *    *    *    *    *    *    *    *
GACGGTGGCC GAGGAGTGGT CCCAGGACCT GCACAGCAGC GGCCGCACGG ACCTCAAGTA
 D G G R G V V P G P A Q Q R P H G P Q V>   80
 T V G E E W S Q D L H S S G R T D L K Y>   80
 * R W A R S G P R T C T A A A A R T S S>   79

       250       260       270       280       290       300
   *    *    *    *    *    *    *    *    *    *    *    *
CTCCTACCGC TTCGTGTGTG ACGAACACTA CTACGGAGAG GGCTGCTCCG TTTTCTGCCG
 L L P L R V * R T L L R R G L L R F L P>  100
 S Y R F V C D E H Y Y G E G C S V F C R>  100
 T P T A S C V T N T T T E R A A P F S A>   99

       310       320       330       340       350       360
   *    *    *    *    *    *    *    *    *    *    *    *
TCCCCGGGAC GATGCCTTCG GCCACTTCAC CTGTGGGGAG CGTGGGGAGA AAGTGTGCAA
 S P G R C L R P L H L W G A W G E S V Q>  120
 P R D D A F G H F T C G E R G E K V C N>  120
 V P G T M P S A T S P V C S V G R K C A>  119
```

FIG.12B1

```
370        380        390        400        410        420
*    *     *    *     *    *     *    *     *    *     *    *
CCCTGGCTGG AAAGGGCCCT ACTGCACAGA GCCGATCTGC CTGCCTGGAT GTGATGAGCA
 P  W  L   E  R  A  L   L  H  R   A  D  L   P  A  W  M   *  *  A>  140
[P  G  W   K  G  P   Y  C  T  E   P  I  C   L  P  G   C  D  E  Q>] 140
T  L  A  G   K  G  P   T  A  Q   S  R  S  A   C  L  D   V  M  S>  139

430        440        450        460        470        480
*    *     *    *     *    *     *    *     *    *     *    *
GCATGGATTT TGTGACAAAC CAGCCCAATG CAAGTGCAGA GTGGGCTGGC AGGGCCGGTA
 A  W  I   L  *  Q  T   R  G  M   Q  V  Q   S  G  L  A   G  P  V>  160
[H  G  F   C  D  K   P  G  E  C   K  C  R   V  G  W  Q   G  R  Y>] 160
S  M  D  F   V  T  N   Q  G  N   A  S  A  E   W  A  G   R  A  G>  159

490        500        510        520        530        540
*    *     *    *     *    *     *    *     *    *     *    *
CTGTGACGAG TGTATCCGCT ATCCAGGCTG TCTCCATGGC ACCTGCCAGC AGCCCTGGCA
 L  *  R   V  Y  P  L   S  R  L   S  P  W   H  L  P  A   A  L  A>  180
[C  D  E   C  I  R   Y  P  G  C   L  H  G   T  C  Q   Q  P  W  Q>] 180
T  V  T  S   V  S  A   I  Q  A   V  S  M  A   P  A  S   S  P  G>  179

550        560        570        580        590        600
*    *     *    *     *    *     *    *     *    *     *    *
GTGCAACTGC CAGGAAGGNT GGGGGGGCCT TTTCTGCAAC CAGGACCTGA ACTACTGCAC
 V  Q  L   P  G  R  X   G  G  P   F  L  Q   P  G  P  E   L  L  H>  200
[C  N  C   Q  E  G   W  G  G  L   F  C  N   Q  D  L   N  Y  C  T>] 200
S  A  T  A   R  K  X   G  G  A   F  S  A  T   R  T  *   T  T  A>  199

610        620        630        640        650        660
*    *     *    *     *    *     *    *     *    *     *    *
ACACCATAAG CCCTGCAAGA ATCGAGCCAC CTGCAACAAA CACGGGCCAG GGGGAGCTAC
 T  P  *   A  L  Q  E   W  S  H   L  Q  Q   T  R  A  R   G [S  Y>]  220
[H  H  K   P  C  K   N  G  A  T   C] N  K   H  G  P   G  G  A  T>  220
H  T  I  S   P  A  R   M  E  P   P  A [T  N   T  G  Q   G] E  L>  219

670        680        690        700        710        720
*    *     *    *     *    *     *    *     *    *     *    *
ACTTGGTCTT TGGCCGGNCT GGGGTACANA GGGTGCCACC TGCGAAGCTT GGGGATTGGA
[T] W  S   L  A  G  L   G  Y  X   G  C  H   L  R  S  L   G  I  G>  240
 L  G  L   W  P  X   W  G  T  X   G  A  T   C  E  A   W  G  L  D>  240
H  L  V  F   G  R  X   C  V  X   R  V  P  P   A  K  L   G  D  W>  239
```

FIG.12B2

```
       730       740       750       760       770       780
        *    *    *    *    *    *    *    *    *    *    *    *
CGAGTTGTTG ACCCCAGCCC TTGGTAAGAA CGGAGGGAGC TTGACGGATC TTCGGAGAAC
 R  V  V  D  P  S  P  W  *  E  R  R  E  L  D  G  S  S  E  N>   260
  E  L  L  T  P  A  L  G  K  N  G  G  S  L  T  D  L  R  R  T>  260
T  S  C  *  P  Q  P  L  V  R  T  E  Q  A  *  R  I  F  G  E>    259

       790       800       810       820       830       840
        *    *    *    *    *    *    *    *    *    *    *    *
AGCTACTCCT GTACCTGCCC ACCCGGCTTC TACGGCAAAA TCTGTGAATT GAGTGCCATG
 S  Y  S  C  T  C  P  P  G  F  Y  G  K  I  C  E  L  S  A  M>   280
  A  T  P  V  P  A  H  P  A  S  T  A  K  S  V  N  *  V  P  *>  280
Q  L  L  L  Y  L  P  T  R  L  L  R  Q  N  L  *  I  E  C  H>    279

       850       860       870       880       890       900
        *    *    *    *    *    *    *    *    *    *    *    *
ACCTGTGCGG ACGGCCCTTG CTTTAACGGG GGTCGGTGCT CAGACAGCCC CGATGGAGGG
 T  C  A  D  G  P  C  F  N  G  G  R  C  S  D  S  P  D  G  G>   300
  P  V  R  T  A  L  A  L  T  G  V  G  A  Q  T  A  P  M  E  G>  300
D  L  C  G  R  P  L  L  *  R  G  S  V  L  R  Q  P  R  W  R>    299

       910       920       930       940       950       960
        *    *    *    *    *    *    *    *    *    *    *    *
TACAGCTGCC GCTGCCCCGT GGGCTACTCC GGCTTCAACT GTGAGAAGAA AATTGACTAC
 Y  S  C  R  C  P  V  G  Y  S  G  F  N  C  E  K  K  I  D  Y>   320
  T  A  A  A  A  P  W  A  T  P  A  S  T  V  R  R  K  L  T  T>  320
V  Q  L  P  L  P  R  G  L  L  R  L  Q  L  *  E  E  N  *  L>    319

       970       980       990      1000      1010      1020
        *    *    *    *    *    *    *    *    *    *    *    *
TGCAGCTCTT CACCCTGTTC TAATGGTGCC AAGTGTGTGG ACCTCGGTGA TGCCTACCTG
 C  S  S  S  P  C  S  N  G  A  K  C  V  D  L  G  D  A  Y  L>   340
  A  A  L  H  P  V  L  M  V  P  S  V  W  T  S  V  M  P  T  C>  340
L  Q  L  F  T  L  F  *  W  C  Q  V  C  G  P  R  *  C  L  P>    339

      1030      1040      1050      1060      1070      1080
        *    *    *    *    *    *    *    *    *    *    *    *
TGCCGCTGCC AGGCCGGCTT CTCGGGGAGG CACTGTGACG ACAACGTGGA CGACTGCGCC
 C  R  C  Q  A  G  F  S  G  R  H  C  D  D  N  V  D  D  C  A>   360
  A  A  A  R  P  A  S  R  G  G  T  V  T  T  T  W  T  T  A  P>  360
V  P  L  P  G  R  L  L  G  E  A  L  *  R  Q  R  G  R  L  R>    359
```

FIG.12B3

```
      1090      1100      1110      1120      1130      1140
         *         *         *         *         *         *
TCCTCCCCGT GCGCCAACGG GGGCACCTGC CGGGATGGCG TGAACGACTT CTCCTGCACC
 S  S  P   C  A  N  G   G  T  C   R  D  G   V  N  D  F   S  C  T>   380
  P  P  R   A  P  T   G  A  P  A   G  M  A   *  T  T   S  P  A  P>  380
L  L  P  V   R  Q  R   G  H  L   P  G  W  R   E  R  L   L  L  H>    379

      1150      1160      1170      1180      1190      1200
         *         *         *         *         *         *
TGCCCGCCTG GCTACACGGG CAGGAACTGC AGTGCCCCCG CCAGCAGGTG CGAGCACGCA
 C  P  P   G  Y  T  G   R  N  C   S  A  P   A  S  R  C   E  H  A>   400
  A  R  L   A  T  R   A  G  T  A   V  P  P   P  A  G   A  S  T  H>  400
L  P  A  W   L  H  G   Q  E  L   Q  C  P  R   Q  Q  V   R  A  R>    399

      1210      1220      1230      1240      1250      1260
         *         *         *         *         *         *
CCCTGCCACA ATGGGGCCAC CTGCCACGAG AGGGGCCACC GCTATNTGTG CGAGTGTGCC
 P  C  H   N  G  A  T   C  H  E   R  G  H   R  Y  X   C  E  C  A>   420
  P  A  T   M  G  P   P  A  T  R   G  A  T   A  I  C   A  S  V  P>  420
T  L  P  Q   W  G  H   L  P  R   E  G  P  P   L  F  V   R  V  C>    419

      1270      1280      1290      1300      1310      1320
         *         *         *         *         *         *
CGAAGCTACG GGGGTCCCAA CTGCCANTTC CTGCTCCCCG AAACTGCCCC CCCGGCCCCA
 R  S  Y   G  G  P  N   C  X  F   L  L  P   E  T  A   P  P  A  P>   440
  E  A  T   G  V  P   T  A  X  S   C  S  P   K  L  P   P  R  P  H>  440
P  K  L  R   G  S  Q   L  P  X   P  A  P  R   N  C  P   P  G  P>    439

      1330      1340      1350      1360      1370      1380
         *         *         *         *         *         *
CGGTGGTGGA AACTCCCCTA AAAAAACCTA AAAGGGCCGG GGGGGGCCCA TCCCCTTGGT
 R  W  W   K  L  P  *   K  N  L   K  G  P   G  G  A  H   P  L  G>   460
  G  G  G   N  S  P   K  K  T  *   K  G  R   G  G  P   I  P  L  V>  460
T  V  V  E   T  P  L   K  K  P   K  R  A  G   G  G  P   S  P  W>    459

      1390      1400      1410      1420      1430      1440
         *         *         *         *         *         *
GGACGTGTGC GCCGGGGTCA TCCTTGTCCT CATGCTGCTG CTGGGCTGTC CCGCTGTGGT
 G  R  V   R  R  G  H   P  C  P   H  A  A   A  G  L  C   R  C  G>   480
  D  V  C   A  G  V   I  L  V  L   M  L  L   L  G  C   A  A  V  V>  480
W  T  C  A   P  G  S   S  L  S   S  C  C  C   W  A  V   P  L  W>    479
```

FIG.12B4

```
        1450      1460      1470      1480      1490      1500
         *    *     *    *     *    *     *    *     *    *     *    *
GGTCTGCGTC CGGCTGAGGC TGCAGAAGCA CCGGCCCCCA GCCGACCCCT GNCGGGGGGA
 G  L  R   P  A  E  A   A  E  A   P  A  P   S  R  P  L   X  G  C>   500
 V  C  V   R  L  R  L   Q  K  H   R  P  P   A  D  P   X  R  G  E>   500
W  S  A  S   G  *  G   C  R  S   T  G  P  Q   P  T  P   X  G  G>   499

        1510      1520      1530      1540      1550      1560
         *    *     *    *     *    *     *    *     *    *     *    *
GACGGAGACC ATGAACAACC TGGNCAACTG CCAGCGTGAG AAGGACATCT CAGTCAGCAT
 D  C  D   H  E  Q  P   G  Q  L   P  A  *   E  G  H  L   S  Q  H>   520
 T  E  T   M  N  N  L   X  N  C   Q  R  E   K  D  I  S   V  S  I>   520
R  R  R  P   *  T  T   W  X  T   A  S  V  R   R  T  S   Q  S  A>   519

        1570      1580      1590      1600      1610      1620
         *    *     *    *     *    *     *    *     *    *     *    *
CATCGGGGNC ACGCAGATCA AGAACACCAA CAAGAAGGCG GACTTCCACG GGGACCACAG
 H  R  G   H  A  D  Q   E  H  Q   Q  E  G   G  L  P  R   G  P  Q>   540
 I  G  X   T  Q  I   K  N  T  N   K  K  A   D  F  H   G  D  H  X>   540
S  S  G  X   R  R  S   R  T  P   T  R  R  R   T  S  T   G  T  T>   539

        1630      1640      1650      1660      1670      1680
         *    *     *    *     *    *     *    *     *    *     *    *
NGCCGACAAG AATGGCTTCA AGGCCCGCTA CCCAGNGGTG GACTATAACC TCGTGCAGGA
 X  R  Q   E  W  L  Q   G  P  L   P  X  G   G  L  *  P   R  A  G>   560
 A  D  K   N  G  F   K  A  R  Y   P  X  V   D  Y  N   L  V  Q  D>   560
X  P  T  R   M  A  S   R  P  A   T  Q  X  W   T  I  T   S  C  R>   559

        1690      1700      1710      1720      1730      1740
         *    *     *    *     *    *     *    *     *    *     *    *
CCTCAAGGGT GACGACACCG CCGTCAGGGA CGCGCACAGC AAGCGTGACA CCAAGTGNCA
 P  Q  G   *  R  H  R   R  Q  G   R  A  Q   Q  A  *  H   Q  V  X>   580
 L  K  G   D  D  T   A  V  R  D   A  H  S   K  R  D   T  K  X  Q>   580
T  S  R  V   T  T  P   P  S  G   T  R  T  A   S  V  T   P  S  X>   579

        1750      1760      1770      1780      1790      1800
         *    *     *    *     *    *     *    *     *    *     *    *
GCCCCAGGGC TCCTCAGGGG AGGAGAAGGG GACCCCCGAC CCACACTCAG GGGGTGGAGG
 A  P  G   L  L  R  G   G  E  G   D  P  R   P  T  L  R   G  W  R>   600
 P  Q  G   S  S  G   E  E  K  G   T  P  D   P  H  S   G  G  G  G>   600
S  P  R  A   P  Q  G   R  R  R   G  P  P  T   H  T  Q   G  V  E>   599
```

FIG.12B5

```
       1810      1820      1830      1840      1850      1860
          *    *    *    *    *    *    *    *    *    *    *    *
AAGCATCTTG AAAGAAAAAG GCCGGACTTC GGGCTTGTTC AACTTTCAAA AGACAANCAA
 K  H  L  E  R  K  R  P  D  F  G  L  V  Q  L  S  K  D  X  Q>  620
  S  I  L  K  E  K  G  R  T  S  G  L  F  N  F  Q  K  T  X  X>  620
E  A  S  *  K  K  K  A  G  L  R  A  C  S  T  F  K  R  Q  X>   619

       1870      1880      1890      1900      1910      1920
          *    *    *    *    *    *    *    *    *    *    *    *
NGTACAAGTC GGTGTNCGTC ATTTCCGNAG GAGGAAGGNT GACTGCGTCA TAGGAANTTG
 X  T  S  R  C  X  S  F  P  X  E  E  G  *  L  R  H  R  X  L>  640
  V  Q  V  G  V  R  H  F  R  R  R  K  X  D  C  V  I  G  X  *>  640
X  Y  K  S  V  X  V  I  S  X  G  G  R  X  T  A  S  *  E  X>   639

       1930      1940      1950      1960      1970      1980
          *    *    *    *    *    *    *    *    *    *    *    *
AGGTNGTAAA NTGGNAGTTG ANNTTGGAAA GNNNTCCCCC GATTCCCNTT TCAAAGTTTT
 R  X  *  X  G  S  *  X  W  K  X  X  P  G  F  R  F  Q  S  F>  660
  G  X  K  X  X  V  X  X  G  K  X  S  P  D  S  X  F  K  V  F>  660
E  V  V  X  W  X  L  X  L  E  X  X  P  R  I  P  X  S  K  F>   659
```

FIG.12B6

```
MOUSE DELTA DNA   GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT GCCGTGGTCT   50
HUMAN DELTA       ---------- ---------- ---------- ---------- ----------

CONSENSUS         GTCCAGCGGT ACCATGGGCC GTCGGAGCGC GCTAGCCCTT GCCGTGGTCT   50

MOUSE DELTA DNA   CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  100
HUMAN DELTA       ---------- ---------- ---------- ---------- ----------

CONSENSUS         CTGCCCTGCT GTGCCAGGTC TGGAGCTCCG GCGTATTTGA GCTGAAGCTG  100

MOUSE DELTA DNA   CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG  150
HUMAN DELTA       ---------- ---------- ---------- ---------- ----------

CONSENSUS         CAGGAGTTCG TCAACAAGAA GGGGCTGCTG GGGAACCGCA ACTGCTGCCG  150

MOUSE DELTA DNA   CGGGGGCTCT GGCCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC  200
HUMAN DELTA       ---------- ---------- ---------- ---------- ----------

CONSENSUS         CGGGGGCTCT GGCCCCGCCTT GCGCCTGCAG GACCTTCTTT CGCGTATGCC  200

MOUSE DELTA DNA   TCAAGCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTACGGC  250
HUMAN DELTA       ---------- ---------- ---------- ---------- ----------

CONSENSUS         TCAAGCACTA CCAGGCCAGC GTGTCACCGG AGCCACCCTG CACCTACGGC  250

MOUSE DELTA DNA   AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTGATGG  300
HUMAN DELTA       ---------- ---------- ---------- ---------- -----CATTG    5

CONSENSUS         AGTGCTGTCA CGCCAGTGCT GGGTGTCGAC TCCTTCAGCC TGCCTSATKG  300

MOUSE DELTA DNA   CGCAGGCATC GACCCC---G CCTTCAGCAA CCCCA--TCC GAT-TC-CCC  343
HUMAN DELTA       GGTACGGGCC CCCCTCGAGG TCGACGGTAT CGATAAGCTT GATATCGAAT   55

CONSENSUS         SGYASGSRYC SMCCYCGAGG YCKWCRGYAW CSMYAAGYYY GATATCGMMY  350

MOUSE DELTA DNA   TTCGGCTTCA CCTGGCCAGG TACCTTCTCT CTGATCATTG AAGCCCTCCA  393
HUMAN DELTA       TCCGGCTTCA CCTGGCCGGG CACCTTCTCT CTGATTATTG AAGCTCTCCA  105

CONSENSUS         TYCGGCTTCA CCTGGCCRGG YACCTTCTCT CTGATYATTG AAGCYCTCCA  400

MOUSE DELTA DNA   TACAGACTCT CCCGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  443
HUMAN DELTA       CACAGATTCT CCTGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  155

CONSENSUS         YACAGAYTCT CCYGATGACC TCGCAACAGA AAACCCAGAA AGACTCATCA  450
```

FIG.13A

MOUSE DELTA DNA	GCCGCCTGAC CACACAGAGG CACCTCACTG TGGGAGAAGA ATGGTCTCAG	493
HUMAN DELTA	GCCGCCTGGC CACCCAGAGG CACCTGACGG TGGGCGAGGA GTGGTCCCAG	205
CONSENSUS	GCCGCCTGRC CACMCAGAGG CACCTSACKG TGGGMGARGA RTGGTCYCAG	500
MOUSE DELTA DNA	GACCTTCACA GTAGCGGCCG CACAGACCTC CGGTACTCTT ACCGCTTTGT	543
HUMAN DELTA	GACCTGCACA GCAGCGGCCG CACGGACCTC AAGTACTCCT ACCGCTTCGT	255
CONSENSUS	GACCTKCACA GYAGCGGCCG CACRGACCTC MRGTACTCYT ACCGSTTYGT	550
MOUSE DELTA DNA	GTGTGACGAG CACTACTACG GAGAAGGTTG CTCTGTGTTC TGCCGACCTC	593
HUMAN DELTA	GTGTGACGAA CACTACTACG GAGAGGGCTG CTCCGTTTTC TGCCGTCCCC	305
CONSENSUS	GTGTGACGAR CACTACTACG GAGARGGYTG CTCYGTKTTC TGCCGWCCYC	600
MOUSE DELTA DNA	GGCATGACGC CTTTGGCCAC TTCACCTGCG GGGACAGAGG GGAGAAGATG	643
HUMAN DELTA	GGCACGATGC CTTCGGCCAC TTCACCTGTG GGGAGCGTGG GGAGAAAGTG	355
CONSENSUS	GGCAYGAYGC CTTYGGCCAC TTCACCTGYG GGGASMGWGG GGAGAARRTG	650
MOUSE DELTA DNA	TGCGACCCTG GCTGGAAAGG CCAGTACTGC GCTGACCCAA TCTGTCTGCC	693
HUMAN DELTA	TGCAACCCTG GCTGGAAAGG GCCCTACTGC ACAGAGCCGA TCTGCCTGCC	405
CONSENSUS	TGCRACCCTG GCTGGAAAGG SCMSTACTGC ACWGASCCRA TCTGYCTGCC	700
MOUSE DELTA DNA	AGGGTGTGAT GACCAACATG GATACTGTGA CAAACCAGGG GAGTGCAAGT	743
HUMAN DELTA	TGGATGTGAT GAGCAGCATG GATTTTGTGA CAAACCAGGG GAATGCAAGT	455
CONSENSUS	WGGRTGTGAT GASCARCATG GATWYTGTGA CAAACCAGGG GARTGCAAGT	750
MOUSE DELTA DNA	GCAGAGTTGG CTGGCAGGGC CGCTACTGCG ATGAGTGCAT CCGATACCCA	793
HUMAN DELTA	GCAGAGTGGG CTGGCAGGGC CGGTACTGTG ACGAGTGTAT CCGCTATCCA	505
CONSENSUS	GCAGAGTKGG CTGGCAGGGC CGSTACTGYS AYGAGTGYAT CCGMTAYCCA	800
MOUSE DELTA DNA	GGTTGTCTCC ATGGCACCTG CCAGCAACCC TGGCAGTGTA ACTGCCAGGA	843
HUMAN DELTA	GGCTGTCTCC ATGGCACCTG CCAGCAGCCC TGGCAGTGCA ACTGCCAGGA	555
CONSENSUS	GGYTGTCTCC ATGGCACCTG CCAGCARCCC TGGCAGTGYA ACTGCCAGGA	850
MOUSE DELTA DNA	AGGCTGGGGG GGCCTTTTCT GCAACCAAGA CCTGAACTAC TGTACTCACC	893
HUMAN DELTA	AGGNTGGGGG GGCCTTTTCT GCAACCAGGA CCTGAACTAC TGCACACACC	605
CONSENSUS	AGGNTGGGGG GGCCTTTTCT GCAACCARGA CCTGAACTAC TGYACWCACC	900

FIG.13B

```
MOUSE DELTA DNA  ATAAGCCGTG CAGGAATGGA GCCACCTGCA -CCAACACGG GCCAGGGG-A   941
HUMAN DELTA      ATAAGCCCTG CAAGAATGGA GCCACCTGCA ACAAACACGG GCCAGGGGGA   655

CONSENSUS        ATAAGCCSTG CARGAATGGA GCCACCTGCA ACMAACACGG GCCAGGGGGA   950

MOUSE DELTA DNA  GCTACACATG TTCCT--GCC -GACCTGGGT ATACA-GGTG CCAACTGTG-   986
HUMAN DELTA      GCTACACTTG GTCTTTGGCC CGNCTGGGGT ACANAGGGTG CCACCTGCGA   705

CONSENSUS        GCTACACWTG KTCYTTGGCC CGNCYKGGGT AYANAGGGTG CCAMCTGYGA  1000

MOUSE DELTA DNA  AGCT--GGAA GTAGATGAG- TG-TGCTCCT AGCCCCT-GC AAGAACGGAG  1031
HUMAN DELTA      AGCTTGGGGA TTGGACGAGT TGTTGACCCC AGCCCTTGGT AAGAACGGAG   755

CONSENSUS        AGCTTGGGRA KTRGAYGAGT TGTTGMYCCY AGCCCYTGGY AAGAACGGAG  1050

MOUSE DELTA DNA  CGAGCTGCAC GGACCTT--G AGGACAGCTT CTCTTGCACC TGCCCTCCCG  1079
HUMAN DELTA      GGAGCTTGAC GGATCTTCGG AGAACAGCTA CTCCTGTACC TGCCCACCCG   805

CONSENSUS        SGAGCTKSAC GGAYCTTCGG AGRACAGCTW CTCYTGYACC TGCCCWCCCG  1100

MOUSE DELTA DNA  GCTTCTATGG CAAGGTCTGT GAGCTGAGCG CCATGACCTG TGCAGATGGC  1129
HUMAN DELTA      GCTTCAACGG CAAAATCTGT GAATTGAGTG CCATGACCTG TGCGGACGGC   855

CONSENSUS        GCTTCTAYGG CAARRTCTGT GARYTGAGYG CCATGACCTG TGCRGAYGGC  1150

MOUSE DELTA DNA  CCTTGCTTCA ATGGAGGACG ATGTTCAGAT AACCCTGACG GAGGCTACAC  1179
HUMAN DELTA      CCTTGCTTTA ACGGGGGTCG GTGCTCAGAC AGCCCCGATG GAGGGTACAG   905

CONSENSUS        CCTTGCTTYA AYGGRGGWCG RTGYTCAGAY ARCCCYGAYG GAGGSTACAS  1200

MOUSE DELTA DNA  CTGCCATTGC CCCTTGGGCT TCTCTGGCTT CAACTGTGAG AAGAAGATGG  1229
HUMAN DELTA      CTGCCGCTGC CCCGTGGGCT ACTCCGGCTT CAACTGTGAG AAGAAAATTG   955

CONSENSUS        CTGCCRYTGC CCCKTGGGCT WCTCYGGCTT CAACTGTGAG AAGAARATKG  1250

MOUSE DELTA DNA  ATCTCTGCGG CTCTTCCCCT TGTTCTAACG GTGCCAAGTG TGTGGACCTC  1279
HUMAN DELTA      ACTACTGCAG CTCTTCACCC TGTTCTAATG GTGCCAAGTG TGTGGACCTC  1005

CONSENSUS        AYYWCTGCRG CTCTTCMCCY TGTTCTAAYG GTGCCAAGTG TGTGGACCTC  1300

MOUSE DELTA DNA  GGCAACTCTT ACCTGTGCCG CTGCCAGGCT GGCTTCTCCG GGAGGTACTG  1329
HUMAN DELTA      GGTGATGCCT ACCTGTGCCG CTGCCAGGCC GGCTTCTCGG GGAGGCACTG  1055

CONSENSUS        GGYRAYKCYT ACCTGTGCCG CTGCCAGGCY GGCTTCTGSG GGAGGYACTG  1350

MOUSE DELTA DNA  CGAGGACAAT GTGGATGACT GTGCCTCCTC CCCGTGTGCA AATGGGGGCA  1379
HUMAN DELTA      TGACGACAAC GTGGACGACT GCGCCTCCTC CCCGTGCGCC AACGGGGGCA  1105

CONSENSUS        YGASGACAAY GTGGAYGACY GYGCCTCCTC CCCGTGYGCM AAYGGGGGCA  1400
```

FIG.13C

```
MOUSE DELTA DNA CCTGCCGGGA CAGTGTGAAC GACTTCTCCT GTACCTGCCC ACCTGGCTAC 1429
HUMAN DELTA     CCTGCCGGGA TGGCGTGAAC GACTTCTCCT GCACCTGCCC GCCTGGCTAC 1155

CONSENSUS       CCTGCCGGGA YRGYGTGAAC GACTTGTCCT GYACCTGCCC RCCYGGCTAC 1450

MOUSE DELTA DNA ACGGGCAAGA ACTGCAGCGC CCCTGTCAGC AGGTGTGAGC ATGCACCCTG 1479
HUMAN DELTA     ACGGGCAGGA ACTGCAGTGC CCCCGCCAGC AGGTGCGAGC ACGCACCCTG 1205

CONSENSUS       ACGGGCARGA ACTGCAGYGC CCCYGYCAGC AGGTGYGAGC AYGCACCCTG 1500

MOUSE DELTA DNA CCATAATGGG GCCACCTGCC ACCAGAGGGG CCAGCGCTAC ATGTGTGAGT 1529
HUMAN DELTA     CCACAATGGG GCCACCTGCC ACGAGAGGGG CCACCGCTAT TTGTGCGAGT 1255

CONSENSUS       CCAYAATGGG GCCACCTGCC ACSAGAGGGG CCASCGCTAY WTGTGYGAGT 1550

MOUSE DELTA DNA GCGCCCAGGG CTATGGCGGC CCCAACTGCC AGTTTCTGCT CCCTG-AGCC 1578
HUMAN DELTA     GTGCCCGAAG CTACGGGGGT CCCAACTGCC ANTTCCTGCT CCCCGAAACT 1305

CONSENSUS       GYGCCCRRRG CTAYGGSGGY CCCAACTGCC ANTTYCTGCT CCCYGAARCY 1600

MOUSE DELTA DNA -ACCACCAGG GCCCATGGTG GTGG-ACCTC AGTGAGAGGC ATAT-GGAGA 1625
HUMAN DELTA     GCCCCCCCGG CCCCACGGTG GTGGAAACTC CCCTAAAAAA ACCTAAAAGG 1355

CONSENSUS       GMCCMCCMGG SCCCAYGGTG GTGGAAMCTC MSYKARARRM AYMTARRAGR 1650

MOUSE DELTA DNA GCCAGGGCGG GCCCTTCCCC TGGGTGGCCG TGTGTGCCGG GGTGGTGCTT 1675
HUMAN DELTA     GCCGGGGGGG GCCCATCCCC TTGGTGGACG TGTGCGCCGG GGTCATCCTT 1405

CONSENSUS       GCCRGGGSGG GCCCWTCCCC TKGGTGGMCG TGTGYGCCGG GGTSRTSCTT 1700

MOUSE DELTA DNA GTCCTCCTGC TGCTGCTGGG CTGTGCTGCT GTGGTGGTCT GCGTCCGGCT 1725
HUMAN DELTA     GTCCTCATGC TGCTGCTGGG CTGTGCCGCT GTGGTGGTCT GCGTCCGGCT 1455

CONSENSUS       GTCCTCMTGC TGCTGCTGGG CTGTGCYGCT GTGGTGGTCT GCGTCCGGCT 1750

MOUSE DELTA DNA GAAGCTACAG AAACACCAGC CTCCATCTGA ACCCTGTGGG GGAGAGACAG 1775
HUMAN DELTA     GAGGCTGCAG AAGCACCGGC CCCCATCCGA CCCCTGNCGG GGGGAGACGG 1505

CONSENSUS       GARGCTRCAG AARCACCRGC CYCCASCYGA MCCCTGNSGG GGRGAGACRG 1800

MOUSE DELTA DNA AAACCATGAA CAACCTAGCC AATTGCCAGC GCGAGAAGGA CGTTTCTGTT 1825
HUMAN DELTA     AGACCATGAA CAACCTGGNC AACTGCCAGC GTGAGAAGGA CATCTCAGTC 1555

CONSENSUS       ARACCATGAA CAACCTRGNC AAYTGCCAGC GYGAGAAGGA CRTYTCWGTY 1850
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FIG. 13D

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MOUSE DELTA DNA  AGCATCATTG GGGCTACCCA GATCAAGAAC ACCAACAAGA AGGCGGACTT  1875
HUMAN DELTA      AGCATCATCG GGGNCACGCA GATCAAGAAC ACCAACAAGA AGGCGGACTT  1605

CONSENSUS        AGCATCATYG GGGNYACSCA GATCAAGAAC ACCAACAAGA AGGCGGACTT  1900

MOUSE DELTA DNA  TCACGGGGAC CATGGAGCCA AGAAGAGCAG CTTTAAGGTC CGATACCCCA  1925
HUMAN DELTA      CCACGGGGAC CACAGNGCCG ACAAGAATGG CTTCAAGGCC CGCTACCCAG  1655

CONSENSUS        YCACGGGGAC CAYRGNGCCR ASAAGARYRG CTTYAAGGYC CGMTACCCMR  1950

MOUSE DELTA DNA  CTGTGGACTA TAACCTCGTT CGAGACCTCA AGGGAGATGA AGCCACGGTC  1975
HUMAN DELTA      NGGTGGACTA TAACCTCGTG CAGGACCTCA AGGGTGACGA CACCGCCGTC  1705

CONSENSUS        NKGTGGACTA TAACCTCGTK CRRGACCTCA AGGGWGAYGA MRCCRCSGTC  2000

MOUSE DELTA DNA  AGGGATACAC ACAGCAAACG TGACACCAAG TGCCAGTCAC AGAGCTCTGC  2025
HUMAN DELTA      AGGGACGCGC ACAGCAAGCG TGACACCAAG TGNCAGCCCC AGGGCTCCTC  1755

CONSENSUS        AGGGAYRCRC ACAGCAAFCG TGACACCAAG TGNCAGYCMC AGRGCTCYKC  2050

MOUSE DELTA DNA  AGGAGAAGAG AA---GATCG CC--CCAACA CTTA-GGGGT GG-GG-AGAT  2067
HUMAN DELTA      AGGGGAGGAG AAGGGGACCC CCGACCCACA CTCAGGGGGT GGAGGAAGCA  1805

CONSENSUS        AGGRGARGAG AAGGGGAYCS CCGACCMACA CTYAGGGGGT GGAGGAAGMW  2100

MOUSE DELTA DNA  TCCTGACAGA AAAAGGCCAG AGTCT--GTC TACTCTACTT TCAAAGGAC-  2113
HUMAN DELTA      TCTTGAAAGA AAAAGGCCGG ACTTCGGGCT TGTTCAACTT TCAAAAGACA  1855

CONSENSUS        TCYTGAMAGA AAAAGGCCRG ASTYYGGGYY TRYTCWACTT TCAAARGACA  2150

MOUSE DELTA DNA  -ACCAAGTAC CAGTCGGTGT ATGTTCTGTC TGCAGAA--A AGGATGAGTG  2160
HUMAN DELTA      ANCAANGTAC AAGTCGGTGT NCGTCATTTC CGNAGGAGGA AGGNTGACTG  1905

CONSENSUS        ANCMANGTAC MAGTCGGTGT NYGTYMTKTC YGNAGRAGGA AGGNTGASTG  2200

MOUSE DELTA DNA  TGTTATA-GC GACTGAGGT- GTAAGATGGA AGCGATGTGG CAAAATTCCC  2208
HUMAN DELTA      CGTCATAGGA ANTTGAGGTN GTAAANTGGN AG---T-TG- --ANNTT---  1945

CONSENSUS        YGTYATAGGM RNYTGAGCTN GTAARNTGGN AGCGATGTGG CAANNTTCCC  2250

MOUSE DELTA DNA  ATTTCTCTCA AATAAAATTC CAAGGATATA GCCCCGATGA ATGCTGCTGA  2258
HUMAN DELTA      ---------GGA AAGNNN-TC CCCGGAT--- --TCCGNT-- ----TTC---  1972

CONSENSUS        ATTTCTCKSA AAKNNNATTC CMMGGATATA GCYCCGNTGA ATGCTKCTGA  2300
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FIG.13E

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MOUSE DELTA DNA GAGAGGAAGG GAGAGGAAAC CCAGGGACTG CTGCTGAGAA CCAGGTTCAG 2308
HUMAN DELTA     ---------- ------AAA- ---------G TTTTT----- ---------- 1981

CONSENSUS       GAGAGGAAGG GAGAGGAAAC CCAGGGACTG YTKYTCAGAA CCAGGTTCAG 2350

MOUSE DELTA DNA GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT 2358
HUMAN DELTA     ---------- ---------- ---------- ---------- ---------- 1981

CONSENSUS       GCGAAGCTGG TTCTCTCAGA GTTAGCAGAG GCGCCCGACA CTGCCAGCCT 2400

MOUSE DELTA DNA AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG 2408
HUMAN DELTA     ---------- ---------- ---------- ---------- ---------- 1981

CONSENSUS       AGGCTTTGGC TGCCGCTGGA CTGCCTGCTG GTTGTTCCCA TTGCACTATG 2450

MOUSE DELTA DNA GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA 2458
HUMAN DELTA     ---------- ---------- ---------- ---------- ---------- 1981

CONSENSUS       GACAGTTGCT TTGAAGAGTA TATATTTAAA TGGACGAGTG ACTTGATTCA 2500

MOUSE DELTA DNA TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA 2508
HUMAN DELTA     ---------- ---------- ---------- ---------- ---------- 1981

CONSENSUS       TATAGGAAGC ACGCACTGCC CACACGTCTA TCTTGGATTA CTATGAGCCA 2550

MOUSE DELTA DNA GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC 2558
HUMAN DELTA     ---------- ---------- ---------- ---------- ---------- 1981

CONSENSUS       GTCTTTCCTT GAACTAGAAA CACAACTGCC TTTATTGTCC TTTTTGATAC 2600

MOUSE DELTA DNA TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT 2608
HUMAN DELTA     ---------- ---------- ---------- ---------- ---------- 1981

CONSENSUS       TGAGATGTGT TTTTTTTTTT CCTAGACGGG AAAAAGAAAA CGTGTGTTAT 2650

MOUSE DELTA DNA TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT 2658
HUMAN DELTA     ---------- ---------- ---------- ---------- ---------- 1981

CONSENSUS       TTTTTTGGGA TTTGTAAAAA TATTTTTCAT GATATCTGTA AAGCTTGAGT 2700

MOUSE DELTA DNA ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA 2708
HUMAN DELTA     ---------- ---------- ---------- ---------- ---------- 1981

CONSENSUS       ATTTTGTGAC GTTCATTTTT TTATAATTTA AATTTTGGTA AATATGTACA 2750
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FIG.13F

MOUSE DELTA DNA	AAGGCACTTC	GGGTCTATGT	GACTATATTT	TTTTGTATAT	AAATGTATTT	2758
HUMAN DELTA	----------	----------	----------	----------	----------	1981
CONSENSUS	AAGGCACTTC	GGGTCTATGT	GACTATATTT	TTTTGTATAT	AAATGTATTT	2800
MOUSE DELTA DNA	ATGGAATATT	GTGCAAATGT	TATTTGAGTT	TTTTACTGTT	TTGTTAATGA	2808
HUMAN DELTA	----------	----------	----------	----------	----------	1981
CONSENSUS	ATGGAATATT	GTGCAAATGT	TATTTGAGTT	TTTTACTGTT	TTGTTAATGA	2850
MOUSE DELTA DNA	AGAAATTCAT	TTTAAAAATA	TTTTTCCAAA	ATAAATATAA	TGAACTACA	2857
HUMAN DELTA	----------	----------	----------	----------	----------	1981
CONSENSUS	AGAAATTCAT	TTTAAAAATA	TTTTTCCAAA	ATAAATATAA	TGAACTACA	2899

FIG.13G

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G F T W P G T F S L I I E A L H T D S P D>     21
D L A T E N P E R L I S R L A T Q R H L>       41
T V G E E W S Q D L H S S G R I D L K Y>       61
S Y R F V C D E H Y Y G E G C S V F C R>       81
P R D D A F G H F T C G E R G E K V C N>      101
P G W K G P Y C T E P I C L P G C D E Q>      121
H G F C D K P G E C K C R V G W Q G R Y>      141
C D E C I R Y P G C L H G T C Q Q P W Q>      161
C N C Q E G W G G L F C N Q D L N Y C T>      181
H H K P C K N G A T C * T N T G Q G *         198
S Y T * P S P * K N G G S L T D L *           213
E N S Y S C T C P P G F Y G K I C E L S A M>  235
T C A D G P C F N G G R C S D S P D G G>      255
Y S C R C P V G Y S G F N C E K K I D Y>      275
C S S S P C S N G A K C V D L G D A Y L>      295
C R C Q A G F S G R H C D D N V D D C A>      315
S S P C A N G G T C R D G V N D F S C T>      335
C P P G Y T G R N C S A P A S R C E H A>      355
P C H N G A T C H E R G H R Y * C E C A>      374
R S Y G G P N C * F L L P E * P P G P *>      391
V V * L L L G C A A V V V C V R L R L Q K H>  412
R P P A D P * R G E T E T M N N L *>          428
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FIG. 14A

N C Q R E K D I S V S I I G * T Q I K N T N> 449

K K A D F H G D H * A D K N G F K A R Y P * 469

V D Y N L V Q D L K G D D T A V R D A H S K R D T K * 494

Q P Q G S S G E E K G T P * P T L R * G G * 514

I * R K R P * S * S T * S K D * T * 526

C V I * E V * 531

FIG. 14B